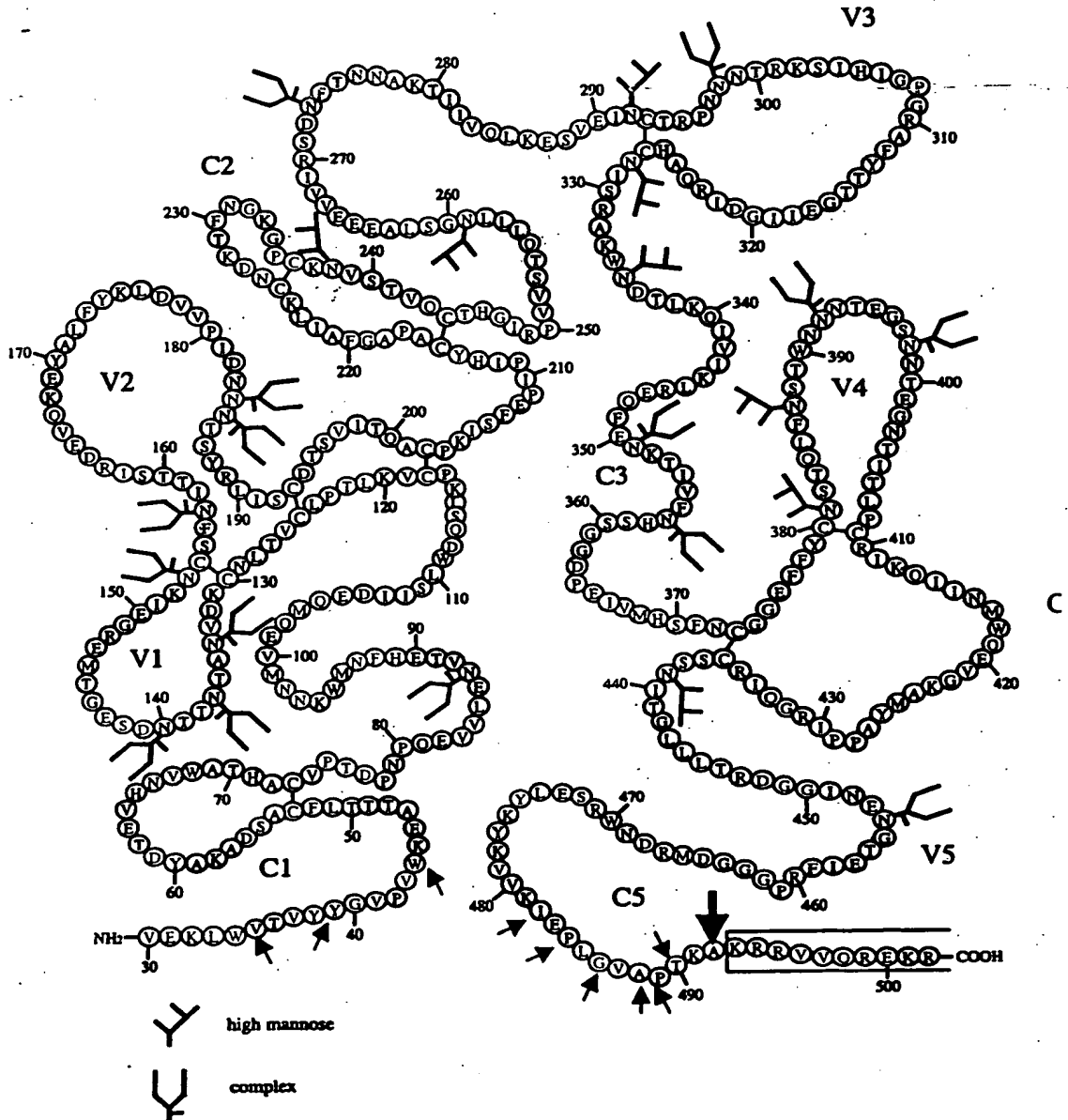


1003291200T

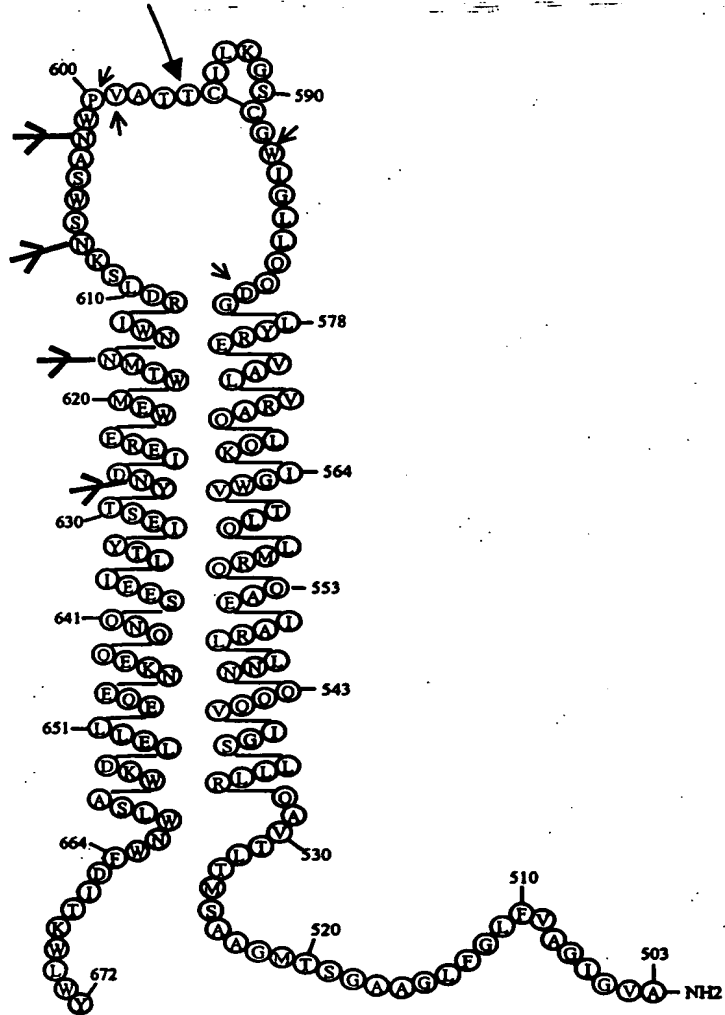


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Figure 3A

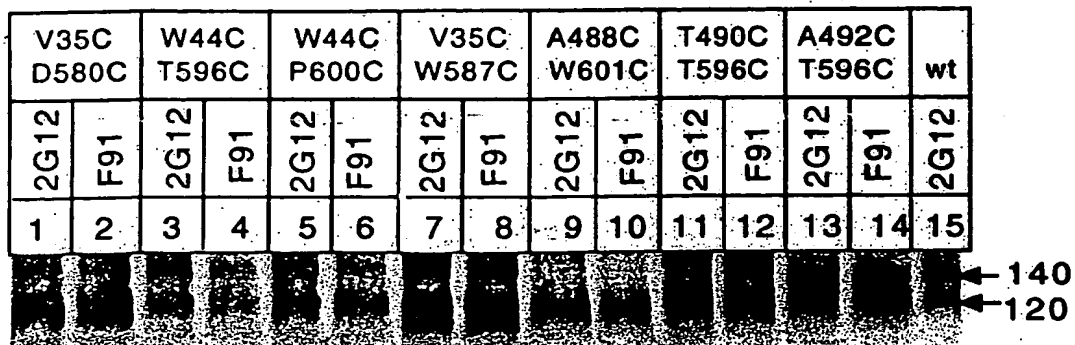


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Figure 3B



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Figure 4



total = 2912000

Figure 5

gp41

	D580C	W587C	T596C	V599C	P600C	W601C
V35C	0.45	0.40	0.35	0.30	0.40	0.30
Y39C	0.35	0.30	0.60	0.45	0.45	N.D.
W44C	0.45	0.45	0.65	0.50	0.65	0.45

gp120

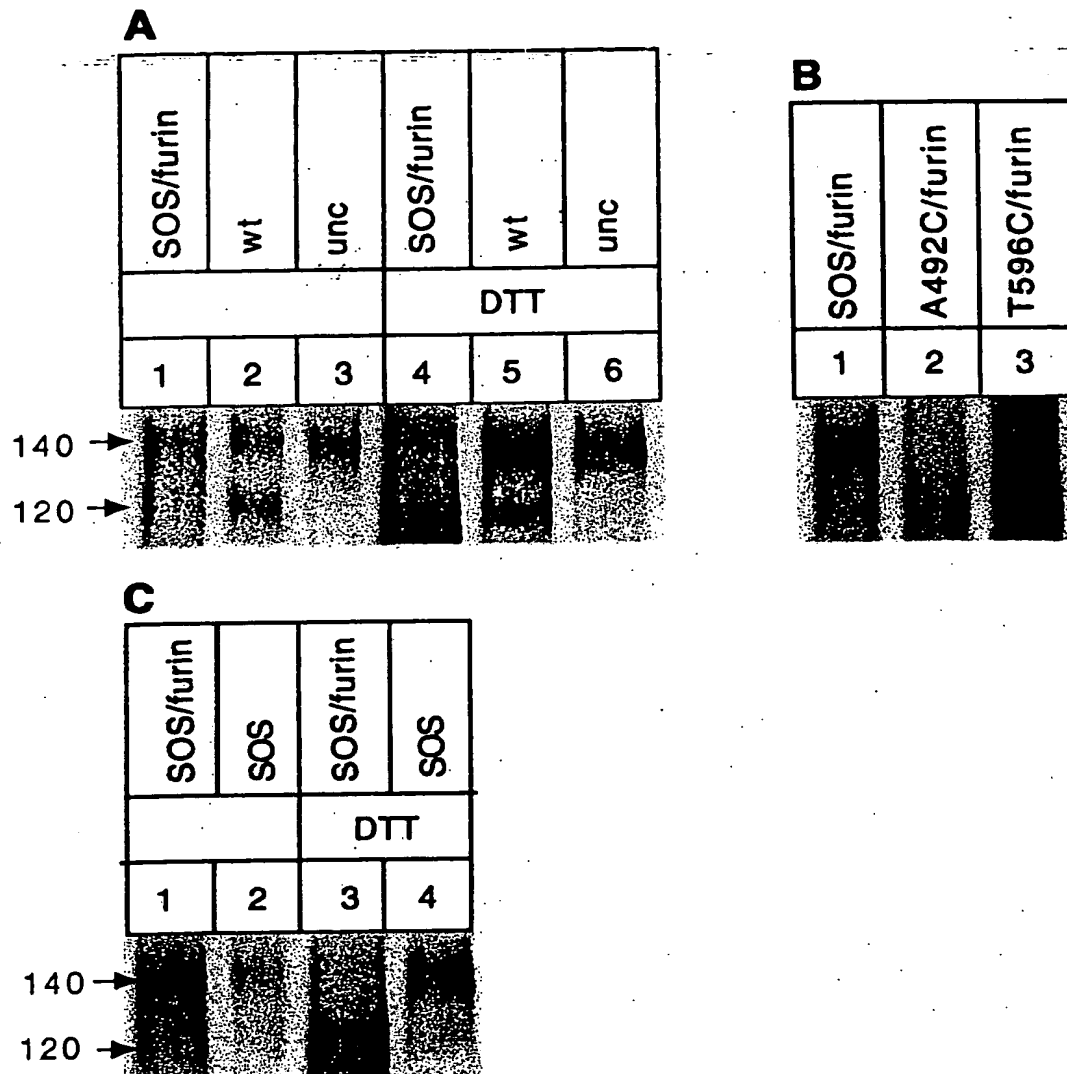
C1

P484C	0.35	0.30	0.45	0	0	0
G486C	0	0	0.25	0.20	0.30	0
A488C	0	0	0.05	0	0	0
P489C	0	0.10	0.30	0.15	0.05	0
T490C	0	0.15	0.55	0.25	0.25	0.10
A492C	0.05	0	0.75	0.50	0.10	0.25

gp120

C5

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Figure 6



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Figure 7

1	490, 596	
2	491, 596	
3	492, 596 (SOS)	
4	493, 596	
5	494, 596	
6	495, 596	
7	496, 596	
8	498, 596	
9	492, 596 (SOS)	K491A
10	492, 596 (SOS)	K493A
11	492, 596 (SOS)	K491A, K493A
12	44, 600; 491, 596	
13	44, 600; 492, 596	
14	44, 600; 493, 596	

140 →
120 →

TOP LEFT = 21372000

Figure 8A

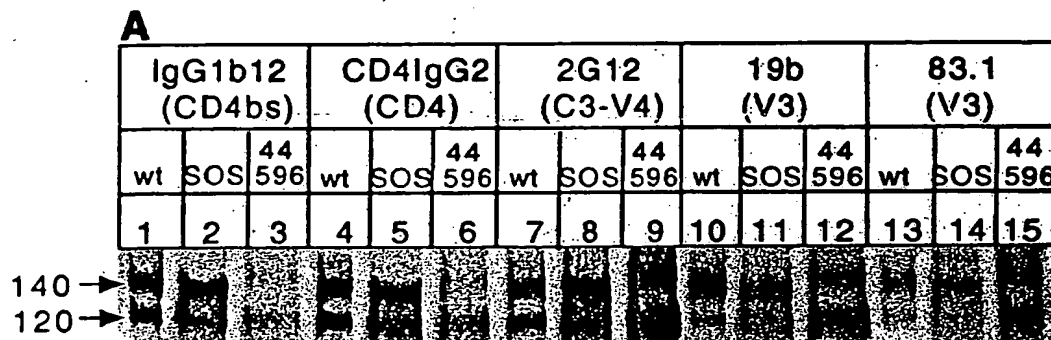


Figure 8B

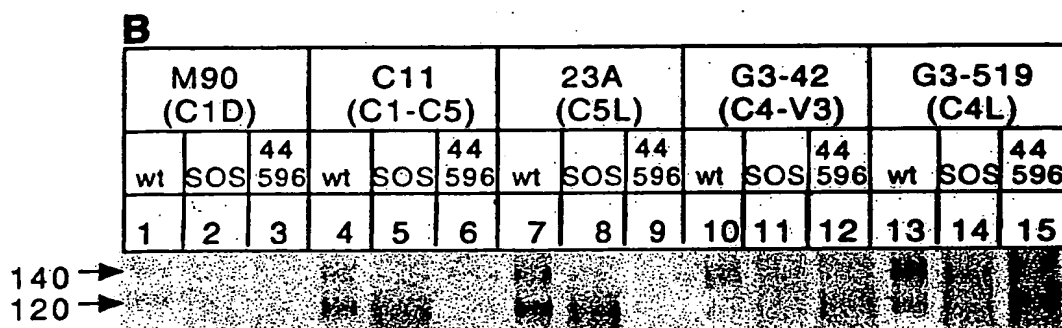


Figure 8C

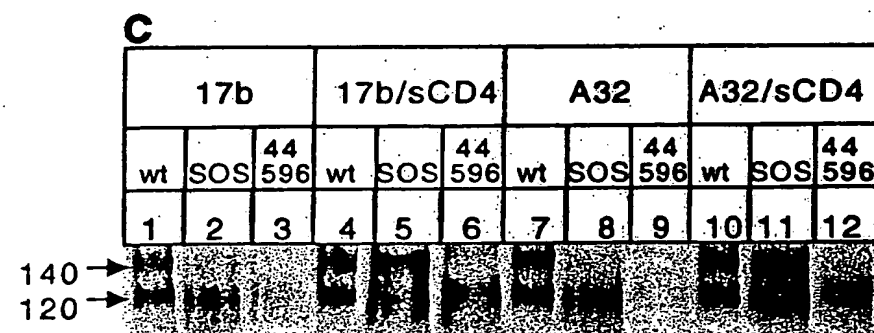
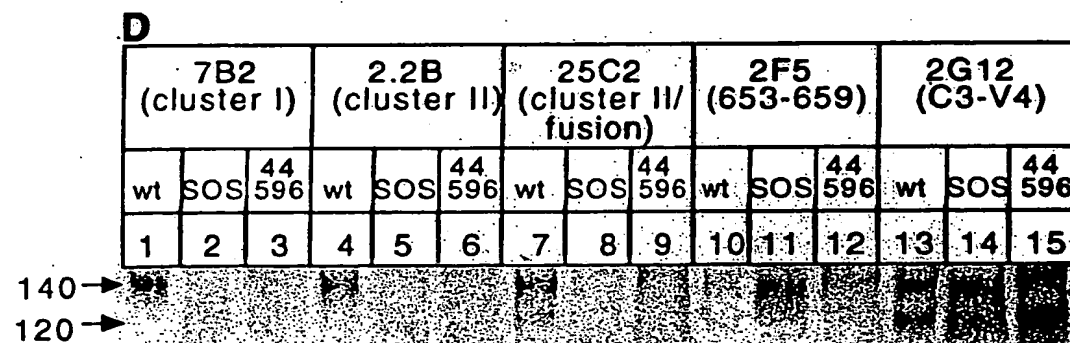
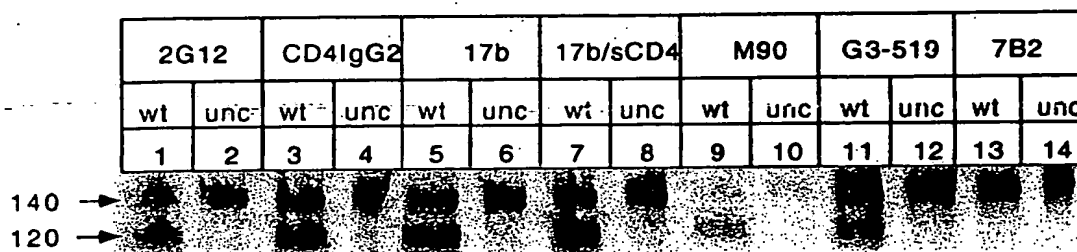


Figure 8D



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Figure 8E



10032163-123404

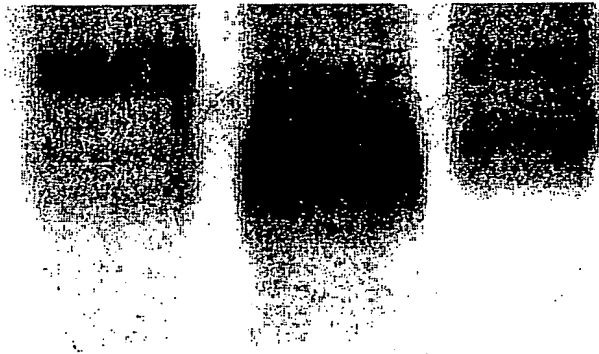
11/20
Figure 9

A

1

2

3



← 140 kDa

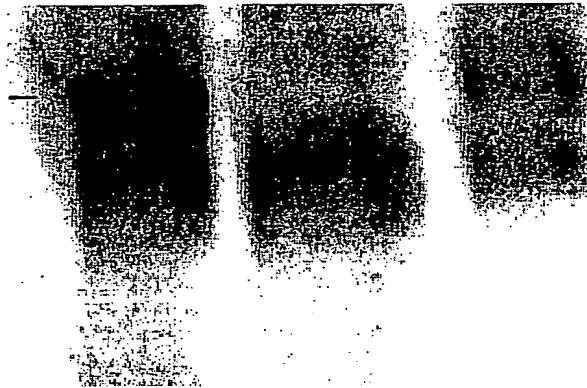
← 120 kDa

B

1

2

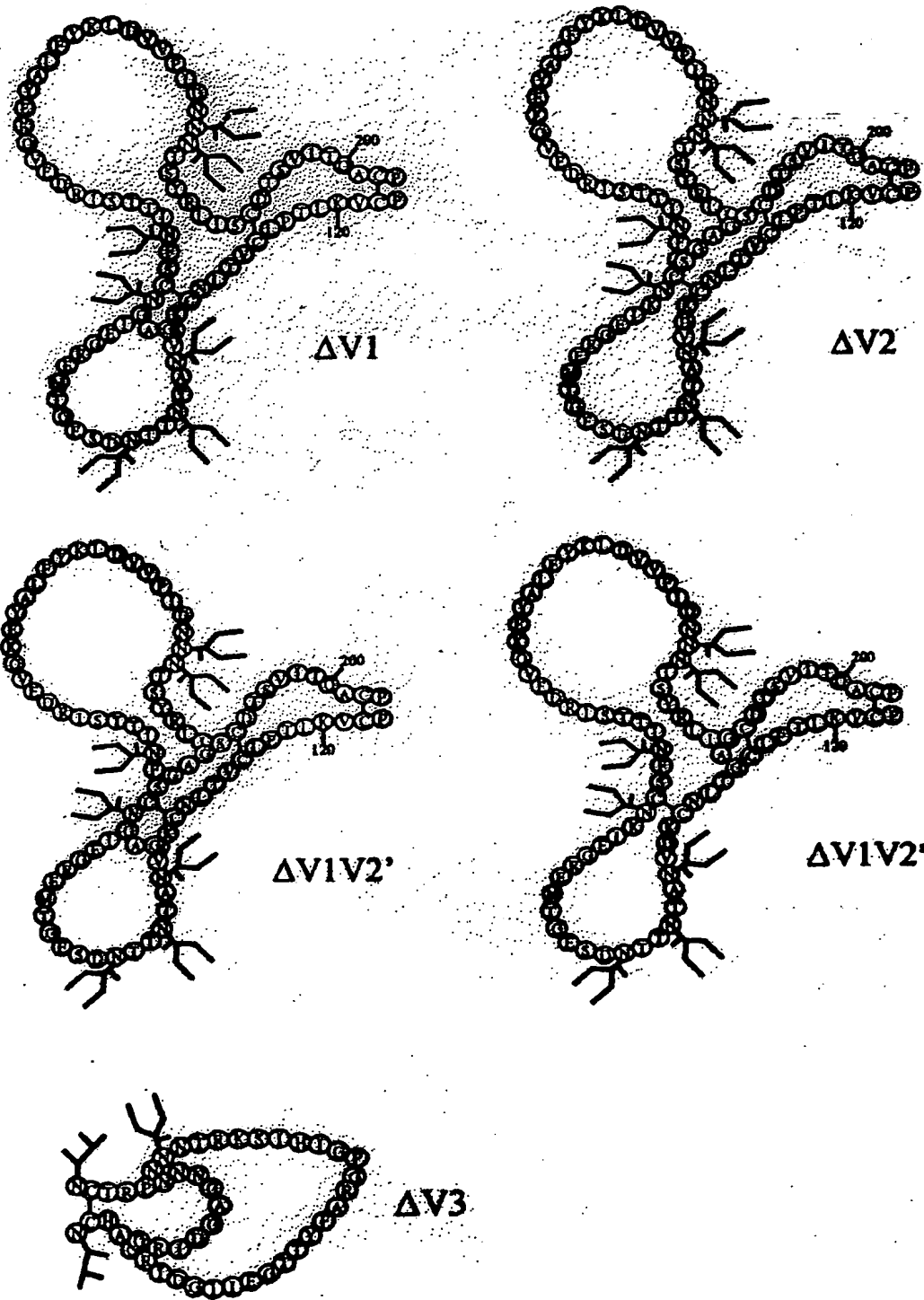
3



← 140 kDa

← 120 kDa

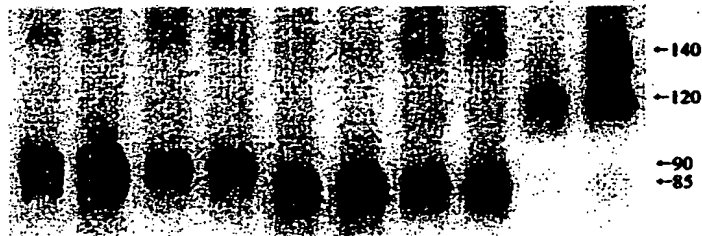
12/20
Figure 10



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Figure 11

A

wt ΔV1V2*V3		CC ΔV1V2*V3		wt ΔV1V2*V3 N357Q N398Q		CC ΔV1V2*V3 N357Q N398Q		wt		envelope protein
2G12	F91	2G12	F91	2G12	F91	2G12	F91	F91	F91	antibody
1	2	3	4	5	6	7	8	9	10	lane



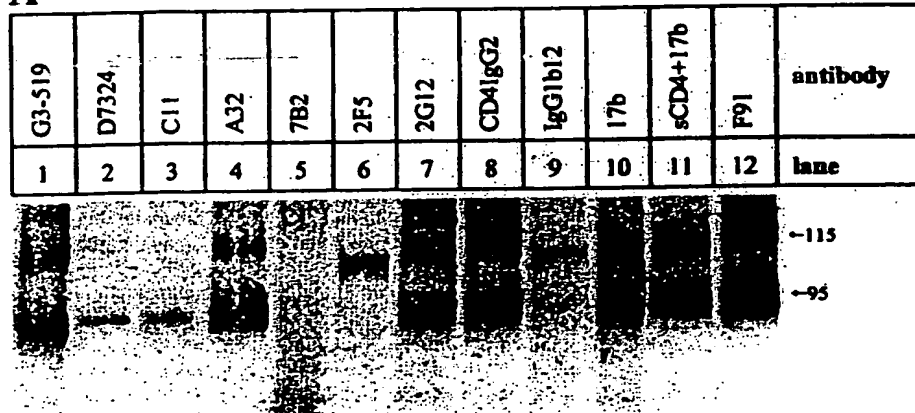
B

wt	ΔV1		ΔV2		ΔV3		ΔV1V2'		ΔV1V2*		ΔV1V2*V3		protein
CC		CC		CC		CC		CC		CC		CC	cysteines
1	2	3	4	5	6	7	8	9	10	11	12	13	lane

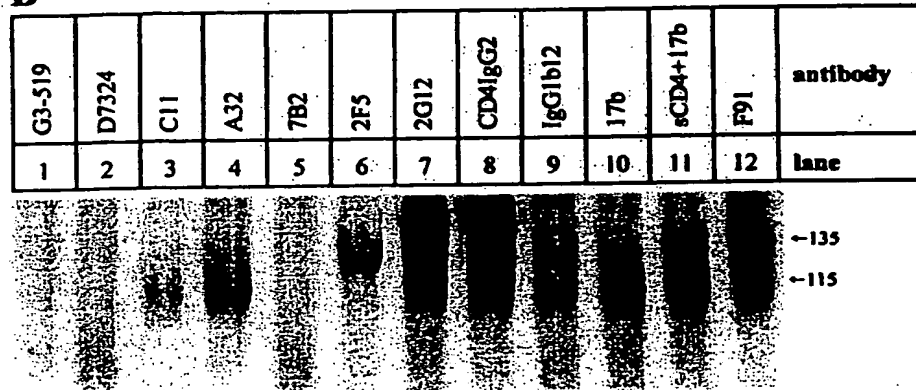


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Figure 12

A



B



HIV-1_{JR-FL} SOS gp140

(a)

1 GTAGAAAAGTTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51 AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAATGTAACAGAACAATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAAT
301 TGCAAGGATGTGAATGCTACTAATAACCACTAATGATAGCGAGGGAACGAT
351 GGAGAGAGGAGAAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401 GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451 CCAATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501 AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATTCCCATAC
551 ATTATTGTGCCCCGGCTGGTTTTGCATTCTAAAGTGTAATGATAAGACG
601 TTCAATGGAAAAGGACCATGTAAAATGTCAGCACAGTACAATGTACACA
651 TGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGGCAGTCTAG
701 CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751 ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801 CAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAGAGCATT
851 ATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAACATT
901 AGTAGAGCAAAATGGAATGACACTTTAAACAGATAGTTATAAAATTAAG
951 AGAACAAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGG
1001 ACCCAGAAATTGTAATGCACAGTTTTAATTGTGAAGGAGAATTTTTCTAC
1051 TGTAATTCAACACAACCTGTTTAATAGTACTTGGAATAATAATACTGAAGG
1101 GTCAAATAACACTGAAGGAAATACTATCACACTCCCATGCAGAATAAAAC
1151 AAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCCTCCC
1201 ATCAGAGGACAAATTAGATGTTCAATCAATATTACAGGGCTGCTATTAAC
1251 AAGAGATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAG
1301 GAGGAGATATGAGGGACAATTGGAGAAGTGAATTCATATAAATATAAAGTA
1351 GTAAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGT
1401 GGTGCAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCCCTTGGGT
1451 TCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACG
1501 GTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAATTT
1551 GCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCACAGTCTGGG
1601 GCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGATACCTAGGG
1651 GATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACCTCATTTGCTG
1701 CACTGCTGTGCCTTGAATGCTAGTTGGAGTAATAAATCTCTAGATAGGA
1751 TTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTAC
1801 ACAAGCGAAATATACACACTAATTGAAGAATCGCAGAACCAACAAGAAAA
1851 GAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATT
1901 GGTTTGACATAACAAACTGGCTGTGGTAT

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNM	VEQMEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNTT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	PIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKGPCKNV	STVQCTHGIR	PVVSTQLLLN	GSLAEEEVVI	RSDNFTNNAK
280	TIIVQLKESV	EINCTRPNNN	TRKSIHIGPG	RAFYTTEGII	GDIRQAHCNI
330	SRAKWNDTLK	QIVIKLREQF	ENKTIVFNHS	SGGDPEIVMH	SFNCEGEFFY
380	CNSTQLFNST	WNNNTEGSNN	TEGNTITLPC	RIKQIINMWQ	EVGKAMYAPP
430	IRGQIRCSSN	ITGLLLTRDG	GINENGTEIF	RPGGGDMRDN	WRSEFYKYKV
480	VKIEPLGVAP	TKCKRRVVQR	EKRAVGIGAV	FLGFLGAAGS	TMGAASMTLT
530	VQARLLLSGI	VQQQNLLRA	IEAQQRLQL	TVWGIKQLQA	RVLAVERYLG
580	DQQLLGIWGC	SGKLICCTAV	PWNASWSNKS	LDRIWNNMTW	MEWEREIDNY
630	TSEIYTLIEE	SONQOEKNEQ	ELLELDKWAS	LWNWFDITNW	LWY

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Figure 14

HIV-1_{JR-FL} ΔV1V2* SOS gp140

(a)

```
1   GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51  AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGGTGCAGGATGT
301 GACACCTCAGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAAT
351 TCCCATACATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGTAATG
401 ATAAGACGTTCAATGGAAAAGGACCATGTAAAAATGTCAGCACAGTACAA
451 TGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGG
501 CAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACA
551 ATGCTAAAACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGT
601 ACAAGACCCAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAG
651 AGCATTTTATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATT
701 GTAACATTAGTAGAGCAAAATGGAATGACACTTTAAAACAGATAGTTATA
751 AAATTAAGAGAACAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTC
801 AGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTGGAGGAGAAT
851 TTTTCTACTGTAATTCAACACAACCTGTTAATAGTACTTGGAATAATAAT
901 ACTGAAGGGTCAAATAACACTGAAGGAAATACTATCACACTCCCATGCAG
951 AATAAAACAAATTATATAACATGTGGCAGGAAGTAGGAAAAGCAATGTATG
1001 CCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTG
1051 CTATTAACAAGAGATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAG
1101 ACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAAT
1151 ATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAG
1201 AGAAGAGTGGTGCAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTT
1251 CCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGA
1301 CACTGACGGTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAG
1351 AACAATTTGCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCAC
1401 AGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT
1451 ACCTAGGGGATCAACAGCTCCTGGGGATTGGGGTTGCTCTGGAAACTC
1501 ATTTGCTGCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCT
1551 GGATAGGATTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTG
1601 ACAATTACACAAGCGAAATATACACCCTAATTGAAGAATCGCAGAACCAA
1651 CAAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTT
1701 GTGGAATTGGTTTGACATAACAACTGGCTGTGGTAT
```

18/20
Figure 14

(b)

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCGAGC
130	DTSVITQACP	KISFEPIPIH	YCAPAGFAIL	KCNDKTFNGK	GPCKNVSTVQ
180	CTHGIRPVVS	TQLLNGSLA	EEEVVIRSDN	FTNNAKTIIV	QLKESVEINC
230	TRPNNNTRKS	IHIGPGRAFY	TTGEIIGDIR	QAHCNISRAK	WNDTLKQIVI
280	KLREQFENKT	IVFNHSSGGD	PEIVMHSFNC	GGEFFYCNST	QLFNSTWNNN
330	TEGSNNTEGN	TITLPCRIKQ	IINMWQEVGK	AMYAPPIRGQ	IRCSSNITGL
380	LLTRDGGINE	NGTEIFRPGG	GDMRDNRWSE	LYKYKVVKIE	PLGVAPTKCK
430	RRVVQREKRA	VGIGAVFLGF	LGAAGSTMGA	ASMTLTVQAR	LLSGIVQQQ
480	NNLLRAIEAQ	QRMLQLTVWG	IKQLQARVLA	VERYLGDQQL	LGIWGCSGKL
530	ICCTAVPWNA	SWSNKSLDRI	WNNMTWMEWE	REIDNYTSEI	YTLIEESQNO
580	QEKNEQELLE	LDKWASLWNW	FDITNWLWY		

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Figure 15

HIV-1_{IR-FL} ΔV3 SOS gp140

(a)

```
1   GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51  AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAAT
301 TGCAAGGATGTGAATGCTACTAATACCACTAATGATAGCGAGGGAACGAT
351 GGAGAGAGGAGAAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401 GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451 CCNATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501 AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATTCCCATAC
551 ATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGTAATGATAAGACG
601 TTCAATGGAAAAGGNCCATGTAAAATGTCAGCACAGTNCAATGTACACA
651 TGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGGCAGTCTAG
701 CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751 ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801 CAACAACAATGGAGCCGGCGATATAAGACAAGCACATTGTAACATTAGTA
851 GAGCAAAATGGAATGACACTTTAAAACAGATAGTTATAAAATTAAGAGAA
901 CAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCC
951 AGAAATTGTAATGCACAGTTTTAATTGTGGAGGAGAATTTTTCTACTGTA
1001 ATTCACACAACCTGTTTAATAGTACTTGGAATAATAATACTGAAGGGTCA
1051 AATAACACTGAAGGAAATACTATCACACTCCCATGCAGAATAAAACAAAT
1101 TATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCCTCCCATCA
1151 GAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTATTAACAAGA
1201 GATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAGGAGG
1251 AGATATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAA
1301 AAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGTGGTG
1351 CAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGTTCTT
1401 GGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACGGTAC
1451 AGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAATTTGCTG
1501 AGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCACAGTCTGGGGCAT
1551 CAAGCAGCTCCAGGCAAGAGTCTTGGCTGTGGAAAGATACCTAGGGGATC
1601 AACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACCTCATTTGCTGCACT
1651 GCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTGGATAGGATTTG
1701 GAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTACACAA
1751 GCGAAATATACACCCTAATTGAAGAATCGCAGAACCAACAAGAAAAGAAT
1801 GAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTT
1851 TGACATAACAAAATGGCTGTGGTAT
```

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80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNTT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	XIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKXPCKNV	STXQCTHGIR	PVVSTQLLL	GSLAEEVVVI	RSDNFTNNAK
280	TIIVQLKESV	EINCTRPNNN	GAGDIRQAH	NISRAKWNDT	LKQIVIKLRE
330	QFENKTIVFN	HSSGGDPEIV	MHSFNCGGEF	FYCNSTQLFN	STWNNNTEGS
380	NNTEGNTITL	PCRIKQIINM	WQEVGKAMYA	PPIRGQIRCS	SNITGLLLTR
430	DGGINENGTE	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKC K RRVV
480	QREKRAVGIG	AVFLGFLGAA	GSTMGAASMT	LTVQARLLLS	GIVQQQNNLL
530	RAIEAQQRML	QLTVWGIKQL	QARVLAVERY	LGDOQLLGIW	GCSGKLIC C T
580	AVPWNASWSN	KSLDRIWNNM	TWMEWEREID	NYTSEIYTLI	EESQNQQEKN
630	EQELLELDKW	ASLWNWFDIT	KWLWY		